Brian D Weitzner

List of Publications by Year
in descending order

19 papers	2,403 citations	623734 14 h-index	794594 19 g-index
22 all docs	22 docs citations	22 times ranked	3800 citing authors

#	Article	IF	Citations
1	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
2	De novo design of potent and selective mimics of IL-2 and IL-15. Nature, 2019, 565, 186-191.	27.8	362
3	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). PLoS ONE, 2013, 8, e63906.	2.5	348
4	Benchmarking and Analysis of Protein Docking Performance in Rosetta v3.2. PLoS ONE, 2011, 6, e22477.	2.5	272
5	Modeling and docking of antibody structures with Rosetta. Nature Protocols, 2017, 12, 401-416.	12.0	236
6	An Integrated Framework Advancing Membrane Protein Modeling and Design. PLoS Computational Biology, 2015, 11, e1004398.	3.2	145
7	RosettaAntibodyDesign (RAbD): A general framework for computational antibody design. PLoS Computational Biology, 2018, 14, e1006112.	3.2	115
8	Blind prediction performance of RosettaAntibody 3.0: Grafting, relaxation, kinematic loop modeling, and full CDR optimization. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1611-1623.	2.6	91
9	The Origin of CDR H3 Structural Diversity. Structure, 2015, 23, 302-311.	3.3	78
10	Real-Time PyMOL Visualization for Rosetta and PyRosetta. PLoS ONE, 2011, 6, e21931.	2.5	55
11	Accurate Structure Prediction of CDR H3 Loops Enabled by a Novel Structure-Based C-Terminal Constraint. Journal of Immunology, 2017, 198, 505-515.	0.8	43
12	Anchor extension: a structure-guided approach to design cyclic peptides targeting enzyme active sites. Nature Communications, 2021, 12, 3384.	12.8	37
13	A computational method for design of connected catalytic networks in proteins. Protein Science, 2019, 28, 2036-2041.	7.6	28
14	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
15	Integration of the Rosetta suite with the python software stack via reproducible packaging and core programming interfaces for distributed simulation. Protein Science, 2020, 29, 43-51.	7.6	13
16	The influence of proline isomerization on potency and stability of anti-HIV antibody 10E8. Scientific Reports, 2020, 10, 14313.	3.3	12
17	A Framework to Simplify Combined Sampling Strategies in Rosetta. PLoS ONE, 2015, 10, e0138220.	2.5	10
18	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8

#	Article	IF	Citations
19	I am a United Academic Worker. Science, 2017, 358, 266-266.	12.6	1